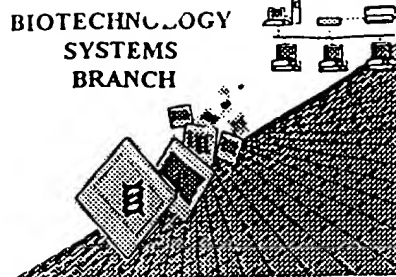


M.T. Davis

## RAW SEQUENCE LISTING ERROR REPORT



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/555,342

Source: 1600

Date Processed by STIC: 10/5/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

### Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

1600

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/555,342

DATE: 10/05/2001

TIME: 13:26:20

Input Set : A:\So5025us.txt

Output Set: N:\CRF3\10052001\I555342.raw

3 <110> APPLICANT: CHUGAI SEIYAKU KABUSHIKI KAISHA  
 5 <120> TITLE OF INVENTION: cDNA and deduced amino acid sequence in human fetus  
 chondrocytes  
 8 <130> FILE REFERENCE: CGS98-04PCT  
 C--> 10 <140> CURRENT APPLICATION NUMBER: US/09/555,342  
 C--> 10 <141> CURRENT FILING DATE: 2000-05-26  
 10 <160> NUMBER OF SEQ ID NOS: 22  
 12 <170> SOFTWARE: PatentIn Ver. 2.0

**Does Not Comply  
 Corrected Diskette Needed**

## ERRORED SEQUENCES

301 <210> SEQ ID NO: 2  
 302 <211> LENGTH: 1045  
 303 <212> TYPE: PRT  
 304 <213> ORGANISM: Homo sapiens  
 306 <400> SEQUENCE: 2  
 307 Met Gly Glu Ile Glu Gln Arg Pro Thr Pro Gly Ser Arg Leu Gly Ala  
 308 1 5 10 15  
 310 Pro Glu Asn Ser Gly Ile Ser Thr Leu Glu Arg Gly Gln Lys Pro Pro  
 311 20 25 30  
 313 Pro Thr Pro Ser Gly Lys Leu Val Ser Ile Lys Ile Gln Met Leu Asp  
 314 35 40 45  
 316 Asp Thr Gln Glu Ala Phe Glu Val Pro Gln Arg Ala Pro Gly Lys Val  
 317 50 55 60  
 319 Leu Leu Asp Ala Val Cys Asn His Leu Asn Leu Val Glu Gly Asp Tyr  
 320 65 70 75 80  
 322 Phe Gly Leu Glu Phe Pro Asp His Lys Lys Ile Thr Val Trp Leu Asp  
 323 85 90 95  
 325 Leu Leu Lys Pro Ile Val Lys Gln Ile Arg Arg Pro Lys His Val Val  
 326 100 105 110  
 328 Val Lys Phe Val Val Lys Phe Phe Pro Pro Asp His Thr Gln Leu Gln  
 329 115 120 125  
 331 Glu Glu Leu Thr Arg Tyr Leu Phe Ala Leu Gln Val Lys Gln Asp Leu  
 332 130 135 140  
 334 Ala Gln Gly Arg Leu Thr Cys Asn Asp Thr Ser Ala Ala Leu Leu Ile  
 335 145 150 155 160  
 337 Ser His Ile Val Gln Ser Glu Ile Gly Asp Phe Asp Glu Ala Leu Asp  
 338 165 170 175  
 340 Arg Glu His Leu Ala Lys Asn Lys Tyr Ile Pro Gln Gln Asp Ala Leu  
 341 180 185 190  
 343 Glu Asp Lys Ile Val Glu Phe His His Asn His Ile Gly Gln Thr Pro  
 344 195 200 205  
 346 Ala Glu Ser Asp Phe Gln Leu Glu Ile Ala Arg Arg Leu Glu Met  
 347 210 215 220  
 349 Tyr Gly Ile Arg Leu His Pro Ala Lys Asp Arg Glu Gly Thr Lys Ile  
 350 225 230 235 240  
 352 Asn Leu Ala Val Ala Asn Thr Gly Ile Leu Val Phe Gln Gly Phe Thr

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/555,342

DATE: 10/05/2001

TIME: 13:26:20

Input Set : A:\So5025us.txt

Output Set: N:\CRF3\10052001\I555342.raw

353				245				250				255		
355	Lys	Ile	Asn	Ala	Phe	Asn	Trp	Ala	Lys	Val	Arg	Lys	Leu	Ser
356				260				265				270		
358	Arg	Lys	Arg	Phe	Leu	Ile	Lys	Leu	Arg	Pro	Asp	Ala	Asn	Ser
359			275				280				285			
361	Gln	Asp	Thr	Leu	Glu	Phe	Leu	Met	Ala	Ser	Arg	Asp	Phe	Cys
362		290					295				300			
364	Phe	Trp	Lys	Ile	Cys	Val	Glu	His	His	Ala	Phe	Phe	Arg	Leu
365	305				310					315				320
367	Glu	Pro	Lys	Pro	Lys	Pro	Lys	Pro	Val	Leu	Phe	Ser	Arg	Gly
368				325				330					335	
370	Phe	Arg	Phe	Ser	Gly	Arg	Thr	Gln	Lys	Gln	Val	Leu	Asp	Tyr
371			340					345				350		
373	Glu	Gly	Gly	His	Lys	Lys	Val	Gln	Phe	Glu	Arg	Lys	His	Ser
374		355					360				365			
376	His	Ser	Ile	Arg	Ser	Leu	Ala	Ser	Gln	Pro	Thr	Glu	Leu	Asn
377		370				375					380			
379	Val	Leu	Glu	Gln	Ser	Gln	Ser	Thr	Ser	Leu	Thr	Phe	Gly	Glu
380	385				390					395				400
382	Ala	Glu	Ser	Pro	Gly	Gln	Ser	Cys	Arg	Arg	Gly	Lys	Glu	Pro
383			405					410					415	
385	Val	Ser	Ala	Gly	Glu	Pro	Gly	Ser	His	Pro	Ser	Pro	Ala	Pro
386			420					425					430	
388	Ser	Pro	Ala	Gly	Asn	Lys	Gln	Ala	Asp	Gly	Ala	Ala	Ser	Ala
389		435					440				445			
391	Glu	Glu	Glu	Glu	Glu	Val	Val	Lys	Asp	Arg	Thr	Gln	Gln	Ser
392		450					455				460			
394	Gln	Pro	Pro	Gln	Pro	Ser	Thr	Gly	Ser	Leu	Thr	Gly	Ser	Pro
395	465				470					475				480
397	Ser	Glu	Leu	Ser	Val	Asn	Ser	Gln	Gly	Gly	Val	Ala	Pro	Ala
398			485					490					495	
400	Thr	Leu	Ser	Pro	Asn	Leu	Ser	Pro	Asp	Thr	Lys	Gln	Ala	Ser
401			500					505					510	
403	Ile	Ser	Pro	Leu	Leu	Asn	Asp	Gln	Ala	Cys	Pro	Arg	Thr	Asp
404		515					520					525		
406	Asp	Glu	Gly	Arg	Arg	Lys	Arg	Phe	Pro	Thr	Asp	Lys	Ala	Tyr
407		530				535					540			
409	Ala	Lys	Glu	Val	Ser	Thr	Glu	Arg	Thr	Tyr	Leu	Lys	Asp	Leu
410	545				550				555					560
412	Val	Ile	Thr	Ser	Trp	Phe	Gln	Ser	Thr	Val	Ser	Lys	Glu	Asp
413				565				570					575	
415	Pro	Glu	Ala	Leu	Lys	Ser	Leu	Ile	Phe	Pro	Asn	Phe	Glu	Pro
416			580					585					590	
418	Lys	Phe	His	Thr	Asn	Phe	Leu	Lys	Glu	Ile	Glu	Gln	Arg	Leu
419		595					600					605		
421	Trp	Glu	Gly	Arg	Ser	Asn	Ala	Gln	Ile	Arg	Asp	Tyr	Gln	Arg
422		610				615					620			
424	Asp	Val	Met	Leu	Lys	Asn	Ile	Gln	Gly	Met	Lys	His	Leu	Ala
425	625				630				635				640	

## RAW SEQUENCE LISTING

DATE: 10/05/2001

PATENT APPLICATION: US/09/555,342

TIME: 13:26:20

Input Set : A:\So5025us.txt

Output Set: N:\CRF3\10052001\I555342.raw

```

427 Leu Trp Lys His Ser Glu Ala Leu Glu Ala Leu Glu Asn Gly Ile Lys
428                               645                               650                               655
430 Ser Ser Arg Arg Leu Glu Asn Phe Cys Arg Asp Phe Glu Leu Gln Lys
431                               660                               665                               670
433 Val Cys Tyr Leu Pro Leu Asn Thr Phe Leu Leu Arg Pro Leu His Arg
434                               675                               680                               685
436 Leu Met His Tyr Lys Gln Val Leu Glu Arg Leu Cys Lys His His Pro
437                               690                               695                               700
439 Pro Ser His Ala Asp Phe Arg Asp Cys Arg Ala Ala Leu Ala Glu Ile
440 705                               710                               715                               720
442 Thr Glu Met Val Ala Gln Leu His Gly Thr Met Ile Lys Met Glu Asn
443                               725                               730                               735
445 Phe Gln Lys Leu His Glu Leu Lys Lys Asp Leu Ile Gly Ile Asp Asn
446                               740                               745                               750
448 Leu Val Val Pro Gly Arg Glu Phe Ile Arg Leu Gly Ser Leu Ser Lys
449                               755                               760                               765
451 Leu Ser Gly Lys Gly Leu Gln Gln Arg Met Phe Phe Leu Phe Asn Asp
452 770                               775                               780
454 Val Leu Leu Tyr Thr Ser Arg Gly Leu Thr Ala Ser Asn Gln Phe Lys
455 785                               790                               795                               800
457 Val His Gly Gln Leu Pro Leu Tyr Gly Met Thr Ile Glu Glu Ser Glu
458                               805                               810                               815
460 Asp Glu Trp Gly Val Pro His Cys Leu Thr Leu Arg Gly Gln Arg Gln
461                               820                               825                               830
463 Ser Ile Ile Val Ala Ala Ser Ser Arg Ser Glu Met Glu Lys Trp Val
464                               835                               840                               845
466 Glu Asp Ile Gln Met Ala Ile Asp Leu Ala Glu Lys Ser Ser Ser Pro
467 850                               855                               860
469 Ala Pro Glu Phe Leu Ala Ser Ser Pro Pro Asp Asn Lys Ser Pro Asp
470 865                               870                               875                               880
472 Glu Ala Thr Ala Ala Asp Gln Glu Ser Glu Asp Asp Leu Ser Ala Ser
473                               885                               890                               895
475 Arg Thr Ser Leu Glu Arg Gln Ala Pro His Arg Gly Asn Thr Met Val
476                               900                               905                               910
478 His Val Cys Trp His Arg Asn Thr Ser Val Ser Met Val Asp Phe Ser
479                               915                               920                               925
481 Ile Ala Val Glu Asn Gln Leu Ser Gly Asn Leu Leu Arg Lys Phe Lys
482 930                               935                               940
484 Asn Ser Asn Gly Trp Gln Lys Leu Trp Val Val Phe Thr Asn Phe Cys
485 945                               950                               955                               960
487 Leu Phe Phe Tyr Lys Ser His Gln Asp Asn His Pro Leu Ala Ser Leu
488                               965                               970                               975
490 Pro Leu Leu Gly Tyr Ser Leu Thr Ile Pro Ser Glu Ser Glu Asn Ile
491                               980                               985                               990
493 Gln Lys Asp Tyr Val Phe Lys Leu His Phe Lys Ser His Val Tyr Tyr
494                               995                               1000                               1005
496 Phe Arg Ala Glu Ser Glu Tyr Thr Phe Glu Arg Trp Met Glu Val Ile
497 1010                               1015                               1020
499 Arg Ser Ala Thr Ser Ser Ala Ser Arg Pro His Val Leu Ser His Lys

```

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/555,342

DATE: 10/05/2001

TIME: 13:26:20

Input Set : A:\So5025us.txt

Output Set: N:\CRF3\10052001\I555342.raw

E--> 500 025 1030 1035 1040  
502 Glu Ser Leu Val Tyr  
503 1045

→ the whole number needs to be on the page, use few amino acids on this line to make number fit.

## VERIFICATION SUMMARY

DATE: 10/05/2001

PATENT APPLICATION: US/09/555,342

TIME: 13:26:21

Input Set : A:\So5025us.txt

Output Set: N:\CRF3\10052001\I555342.raw

L:10 M:270 C: Current Application Number differs, Replaced Current Application No  
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:500 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:2  
L:508 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:3  
L:512 M:283 W: Missing Blank Line separator, <400> field identifier  
L:518 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:4  
L:522 M:283 W: Missing Blank Line separator, <400> field identifier  
L:528 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:5  
L:532 M:283 W: Missing Blank Line separator, <400> field identifier  
L:538 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:6  
L:542 M:283 W: Missing Blank Line separator, <400> field identifier  
L:548 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:7  
L:552 M:283 W: Missing Blank Line separator, <400> field identifier  
L:558 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:8  
L:562 M:283 W: Missing Blank Line separator, <400> field identifier  
L:568 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:9  
L:572 M:283 W: Missing Blank Line separator, <400> field identifier  
L:578 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:10  
L:582 M:283 W: Missing Blank Line separator, <400> field identifier  
L:588 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:11  
L:592 M:283 W: Missing Blank Line separator, <400> field identifier  
L:598 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:12  
L:602 M:283 W: Missing Blank Line separator, <400> field identifier  
L:608 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:13  
L:612 M:283 W: Missing Blank Line separator, <400> field identifier  
L:618 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:14  
L:622 M:283 W: Missing Blank Line separator, <400> field identifier  
L:628 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:15  
L:632 M:283 W: Missing Blank Line separator, <400> field identifier  
L:638 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:16  
L:642 M:283 W: Missing Blank Line separator, <400> field identifier  
L:648 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:17  
L:652 M:283 W: Missing Blank Line separator, <400> field identifier  
L:658 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:18  
L:662 M:283 W: Missing Blank Line separator, <400> field identifier  
L:668 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:19  
L:672 M:283 W: Missing Blank Line separator, <400> field identifier  
L:678 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:20  
L:682 M:283 W: Missing Blank Line separator, <400> field identifier  
L:688 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:21  
L:692 M:283 W: Missing Blank Line separator, <400> field identifier  
L:698 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:22  
L:702 M:283 W: Missing Blank Line separator, <400> field identifier